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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/032,827A

DATE: 05/01/2002
TIME: 12:01:18

Input Set : A:\seqlistcorrected.txt
Output Set: N:\CRF3\05012002\J032827A.raw

3 <110> APPLICANT: Schwartz, John J.
4 Jacobson, Joseph
5 Dasgupta, Ruchira
7 <120> TITLE OF INVENTION: Engineered Stimulus-Responsive Switches
9 <130> FILE REFERENCE: ENZ-004
11 <140> CURRENT APPLICATION NUMBER: US 10/032,827A
12 <141> CURRENT FILING DATE: 2001-10-23
14 <150> PRIOR APPLICATION NUMBER: US 60/242,546
15 <151> PRIOR FILING DATE: 2000-10-23
17 <160> NUMBER OF SEQ ID NOS: 20
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 21
23 <212> TYPE: PRT
C--> 24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Zinc finger consensus sequence
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: (2)..(3)
32 <223> OTHER INFORMATION: wherein Xaa at positions 2, 3 can be any amino acid
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (5)..(7)
38 <223> OTHER INFORMATION: wherein Xaa at positions 5, 6, 7 can be any amino acid
41 <220> FEATURE:
42 <221> NAME/KEY: misc_feature
43 <222> LOCATION: (9)..(13)
44 <223> OTHER INFORMATION: wherein Xaa at positions 9, 10, 11, 12, 13 can be any amino acid
47 <220> FEATURE:
48 <221> NAME/KEY: misc_feature
49 <222> LOCATION: (15)..(16)
50 <223> OTHER INFORMATION: wherein Xaa at positions 15, 16 can be any amino acid
53 <220> FEATURE:
54 <221> NAME/KEY: misc_feature
55 <222> LOCATION: (18)..(20)
56 <223> OTHER INFORMATION: wherein Xaa at positions 18, 19, 20 can be any amino acid
59 <400> SEQUENCE: 1
W--> 61 Cys Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
62 1 5 10 15
W--> 64 His Xaa Xaa Xaa His
65 20
67 <210> SEQ ID NO: 2

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68 <211> LENGTH: 22
69 <212> TYPE: PRT
C--> 70 <213> ORGANISM: Artificial
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Zinc finger consensus sequence
75 <220> FEATURE:
76 <221> NAME/KEY: misc_feature
77 <222> LOCATION: (2)..(4)
78 <223> OTHER INFORMATION: wherein Xaa at positions 2, 3, 4 can be any amino acid
81 <220> FEATURE:
82 <221> NAME/KEY: misc_feature
83 <222> LOCATION: (6)..(8)
84 <223> OTHER INFORMATION: wherein Xaa at positions 6, 7, 8 can be any amino acid
87 <220> FEATURE:
88 <221> NAME/KEY: misc_feature
89 <222> LOCATION: (10)..(14)
90 <223> OTHER INFORMATION: wherein Xaa at positions 10, 11, 12, 13, 14 can be any amino acid
93 <220> FEATURE:
94 <221> NAME/KEY: misc_feature
95 <222> LOCATION: (16)..(17)
96 <223> OTHER INFORMATION: wherein Xaa at positions 16, 17 can be any amino acid
99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (19)..(21)
102 <223> OTHER INFORMATION: wherein Xaa at positions 19, 20, 21 can be any amino acid
105 <400> SEQUENCE: 2
W--> 107 Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Leu Xaa
108 1 5 10 15
W--> 110 Xaa His Xaa Xaa Xaa His
111 20
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 23
115 <212> TYPE: PRT
C--> 116 <213> ORGANISM: Artificial
118 <220> FEATURE:
119 <223> OTHER INFORMATION: Zinc finger consensus sequence
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
123 <222> LOCATION: (2)..(5)
124 <223> OTHER INFORMATION: wherein Xaa at positions 2, 3, 4, 5 can be any amino acid
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (7)..(9)
130 <223> OTHER INFORMATION: wherein Xaa at positions 7, 8, 9 can be any amino acid
133 <220> FEATURE:
134 <221> NAME/KEY: misc_feature
135 <222> LOCATION: (11)..(15)
136 <223> OTHER INFORMATION: wherein Xaa at positions 11, 12, 13, 14, 15 can be any amino acid
139 <220> FEATURE:

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140 <221> NAME/KEY: misc_feature
141 <222> LOCATION: (17)..(18)
142 <223> OTHER INFORMATION: wherein Xaa at positions 17, 18 can be any amino acid
145 <220> FEATURE:
146 <221> NAME/KEY: misc_feature
147 <222> LOCATION: (20)..(22)
148 <223> OTHER INFORMATION: wherein Xaa at positions 20, 21, 22 can be any amino acid
151 <400> SEQUENCE: 3

W--> 153 Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Leu
154 1 5 10 15

W--> 156 Xaa Xaa His Xaa Xaa Xaa His

157 20

159 <210> SEQ ID NO: 4

160 <211> LENGTH: 21

161 <212> TYPE: PRT

C--> 162 <213> ORGANISM: Artificial

164 <220> FEATURE:

165 <223> OTHER INFORMATION: Zinc finger consensus sequence

167 <220> FEATURE:

168 <221> NAME/KEY: misc_feature

169 <222> LOCATION: (2)..(3)

170 <223> OTHER INFORMATION: wherein Xaa at positions 2, 3 can be any amino acid

173 <220> FEATURE:

174 <221> NAME/KEY: misc_feature

175 <222> LOCATION: (4)..(16)

176 <223> OTHER INFORMATION: wherein Xaa at positions 5, 6, 7, 8, 9, 10, 11, 12, 13, 14,

15, 1
177 6, 17 can be any amino aci
180 <220> FEATURE:
181 <221> NAME/KEY: misc_feature
182 <223> OTHER INFORMATION: wherein Xaa at positions 19, 20 can be any amino acid
185 <400> SEQUENCE: 4

W--> 187 Cys Xaa Xaa Cys Xaa
188 1 5 10 15

W--> 190 Xaa Cys Xaa Xaa Cys

191 20

193 <210> SEQ ID NO: 5

194 <211> LENGTH: 7

195 <212> TYPE: PRT

C--> 196 <213> ORGANISM: Artificial

198 <220> FEATURE:

199 <223> OTHER INFORMATION: target sequence for protein kinase A

201 <400> SEQUENCE: 5

203 Leu Arg Arg Ala Ser Leu Gly

204 1 5

206 <210> SEQ ID NO: 6

207 <211> LENGTH: 10

208 <212> TYPE: PRT

C--> 209 <213> ORGANISM: Artificial

211 <220> FEATURE:

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212 <223> OTHER INFORMATION: substrate for casein kinase II

214 <400> SEQUENCE: 6

216 Arg Arg Arg Glu Glu Glu Thr Glu Glu

217 1 5 10

219 <210> SEQ ID NO: 7

220 <211> LENGTH: 12

221 <212> TYPE: PRT

C--> 222 <213> ORGANISM: Artificial

224 <220> FEATURE:

225 <223> OTHER INFORMATION: substrate sequence for v-Abl tyrosine kinase

227 <400> SEQUENCE: 7

229 Glu Ala Ile Tyr Ala Ala Pro Phe Ala Lys Lys Lys

230 1 5 10

232 <210> SEQ ID NO: 8

233 <211> LENGTH: 27

234 <212> TYPE: DNA

C--> 235 <213> ORGANISM: Artificial

237 <220> FEATURE:

238 <223> OTHER INFORMATION: primer for leucine zipper motif

240 <400> SEQUENCE: 8

241 atcgcgcaca tgaaacaact tgaagac

27

244 <210> SEQ ID NO: 9

245 <211> LENGTH: 22

246 <212> TYPE: DNA

C--> 247 <213> ORGANISM: Artificial

249 <220> FEATURE:

250 <223> OTHER INFORMATION: primer for leucine zipper motif

252 <400> SEQUENCE: 9

253 tcaqcgttcg ccaactaatt tc

22

256 <210> SEQ ID NO: 10

257 <211> LENGTH: 26

258 <212> TYPE: DNA

C--> 259 <213> ORGANISM: Artificial

261 <220> FEATURE:

262 <223> OTHER INFORMATION: primer for lambda repressor

264 <400> SEQUENCE: 10

265 atgagcacaa aaaagaaacc attaac

26

268 <210> SEQ ID NO: 11

269 <211> LENGTH: 18

270 <212> TYPE: DNA

C--> 271 <213> ORGANISM: Artificial

273 <220> FEATURE:

274 <223> OTHER INFORMATION: primer for lambda repressor

276 <400> SEQUENCE: 11

277 qcttacccag cgctccgc

18

280 <210> SEQ ID NO: 12

281 <211> LENGTH: 504

282 <212> TYPE: DNA

C--> 283 <213> ORGANISM: Artificial

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Input Set : A:\seqlistcorrected.txt
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285 <220> FEATURE:
286 <223> OTHER INFORMATION: CI-bZIP repressor variant
288 <400> SEQUENCE: 12
289 atggagcacaa aaaagaaaacc attaacacaa gagcagcttg aggacgcacg tcgccttaaa 60
291 qcaattttatg aaaaaaaaagaa aaatgaactt ggcttatccc aggaatctgt cgccagacaag 120
293 atggggatgg ggcagtctagg ctgtgggtct ttatattaatg gcatcaatgc attaaatgct 180
295 tataacgcgg cattgtttac aaaaattctc aaagtttagcg ttgaagaatt tagcccttca 240
297 atcgccagag aaatctacga gatgtatgaa gcggtagta tgcagccgtc acttagaagt 300
299 qagttatgagt accctgtttt ttctcatgtt caggcaggga tggcttcacc taagctttaga 360
301 acctttacca aaggtgatgc ggagcgctgg gtaagcatcg cgccatcgaa acaacttggaa 420
303 gacaagggtg aagaattgct ttcgaaaaat tatcaacttgg aaaatgaggt tgccagatta 480
305 aqaaatttag ttggcgaacg ctga 504
308 <210> SEQ ID NO: 13
309 <211> LENGTH: 35
310 <212> TYPE: DNA
C--> 311 <213> ORGANISM: Artificial
313 <220> FEATURE:
314 <223> OTHER INFORMATION: primer for coding sequence of a temperature sensitive form of the
315 lambda repressor containing an Aval sit
317 <400> SEQUENCE: 13
318 ttacaacgcc cgggtcagcc aaacgtctct tcagg 35
321 <210> SEQ ID NO: 14
322 <211> LENGTH: 71
323 <212> TYPE: DNA
C--> 324 <213> ORGANISM: Artificial
326 <220> FEATURE:
327 <223> OTHER INFORMATION: primer for the coding sequence of a temperature sensitive form of
328 lambda represso
330 <400> SEQUENCE: 14
331 atgggcattt tctcgagtca gccgggcat accccgcattt cggcggccag cacaaaaaaag 60
333 aaaccattaa c 71
336 <210> SEQ ID NO: 15
337 <211> LENGTH: 784
338 <212> TYPE: DNA
C--> 339 <213> ORGANISM: Artificial
341 <220> FEATURE:
342 <223> OTHER INFORMATION: TBD-CI chimeric repressor variant
344 <400> SEQUENCE: 15
345 atgggcattt tctcgagtca gccgggcat accccgcattt cattaacaca agagcagcac 60
347 aaaaaaaaagaa ccattaacac aagagcagct tgaggacgca cgtcgccctt aagcaattt 120
349 taaaaaaaag aaaaatgaac ttggcttattt ccagaatct gtcgcagaca agatggggat 180
351 qgggcagtca ggcgtgggtc ttatattaa tggcatcaat gcatatggat cttataacgc 240
353 ccattgtttt acaaaaattt tcaaaatgtt cgttggaa tttggccctt caatcgccag 300
355 aqaaatctac gagatgtatg aagcggttag tatgcagccg tcacttagaa gtgagttatg 360
357 gtaccctgtt catcaccatc accatcaattt ttctcatgtt caggcaggga tggcttcacc 420
359 taagctttaga acctttacca aaggtgatgc ggagagatgg gtaagcaca acaaaaaaagc 480
361 cagtgattct gcattctggc ttgaggttga aggttattcc atgaccgcac caacaggctc 540
363 caagccaagc ttccctgacg gaatgttaat tctcggttac cctgagcagg ctgttgagcc 600
365 aqgtgatttc tgcatagcca gacttgggg tgatgagttt accttcaaga aactgatcag 660

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3,5,6,7,9,10,11,12,13,15,16,18,19,20
Seq#:2; Xaa Pos. 2,3,4,6,7,8,10,11,12,13,14,16,17,19,20,21
Seq#:3; Xaa Pos. 2,3,4,5,7,8,9,11,12,13,14,15,17,18,20,21,22
Seq#:4; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,19,20

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20

VERIFICATION SUMMARY

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Input Set : A:\seqlistcorrected.txt

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L:24 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
L:70 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:16
L:116 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16
L:162 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
L:196 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:209 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:222 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:247 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:259 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:271 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:283 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:311 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:324 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:339 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:377 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:392 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:422 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:450 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:463 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20